Using post-mortem surveillance data to investigate liver fluke (*Fasciola hepatica*) infection levels in Northern Ireland

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Objectives

Liver fluke (*Fasciola hepatica*) is a widespread and common parasite of ruminants. Liver fluke infection status (for non-clinical cases) at the animal level is captured during meat inspection of all animals processed for human consumption within Northern Ireland. These large datasets have not been analysed recently to assess their utility in uncovering trends in fluke infection at animal and herd levels in Northern Ireland. Furthermore, these data could be a useful source of information for other hypotheses, including co-infection dynamics.

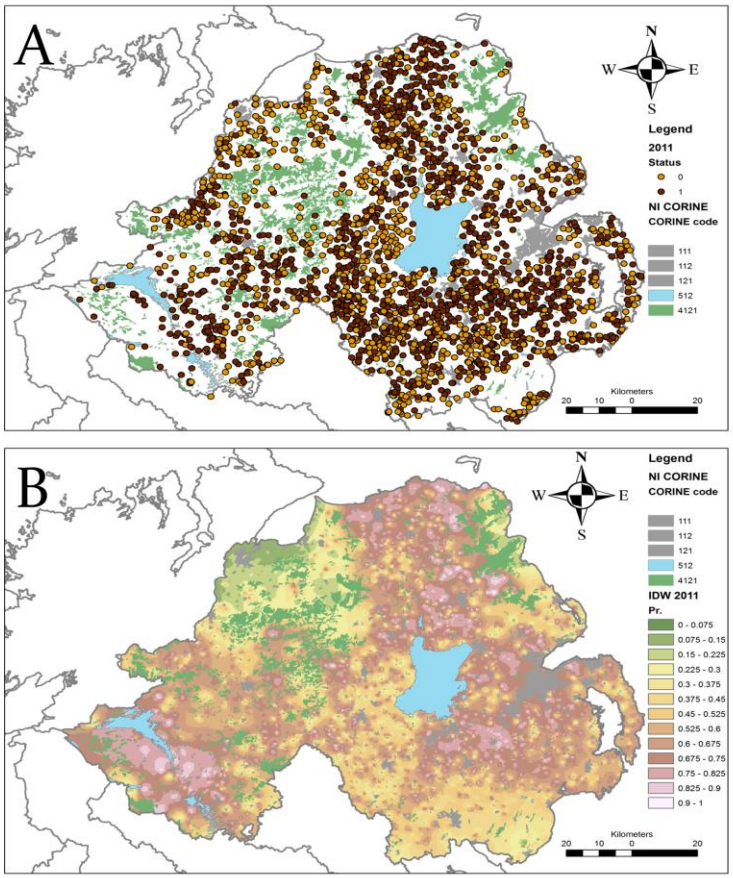

Figure 1. A. Point map of the severely infected (top quartile; status = 1) farms and the non-severely fluke infected farms (bottom quartile; status = 0) in Northern Ireland in 2011. **B.** Raster map of the predicted within herd prevalence in Northern Ireland in 2011. The CORINE land cover types presented in this map correspond with: 111=Continuous urban fabric; 112 = Discontinuous urban fabric; 121 = Industrial and commercial units; 512 = Water bodies; 4121 = Unexploited bogs.

Materials and Methods

We utilised a dataset of ***1.2 million animal records from 18000 herds across three years*** (2011-2013; Fig 1A) to assess ***animal and herd level apparent prevalence*** and risk factors associated with fluke infection. Data from routine meat inspection surveillance were gathered from the Animal and Public Health Information System (APHIS) for Northern Ireland. Appropriate data cleaning was undertaken before exploratory descriptive analysis. Animal level prevalence was measured as the proportion of animals exhibiting evidence of fluke infection at slaughter; herd-level infection prevalence was measured by categorising herds into infected or not (binary), if at least one animal exhibited of fluke infection at slaughter per unit time. "Within herd" infection prevalence was measured using the proportion of animals within a herd that showed evidence of fluke infection (ranging from 0-1), with the inclusion criteria of a minimum of 13 animals sampled per herd per year. "Within herd" infection prevalence at the herd level was investigated using logistic regression, Generalised Linear models (GLM) and Fractional Response Regression (FRR), with spatial patterns presented using Geographic Information Systems (GIS).

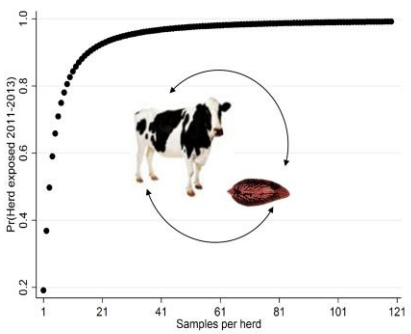

Figure 2: The relationship between the probability of a herd having evidence of fluke infection and the number of animals slaughtered per herd in Northern Ireland 2011-2013.

Results

At the ***animal level***, the proportion of animals slaughtered that exhibited evidence of infection varied between ***20-25%*** amongst years. ***Across herds***, the proportion of herds with at least one infected animal, varied between ***60-65%***. There was, however, a significant sampling effect at the herd-level (Fig. 2); all herds where at least 105 animals slaughtered over the study period exhibited evidence of fluke exposure (100%). There was significant variation in within-herd infection prevalence risk as elucidated by GLMs and FRRs. ***Risk factors*** included ***herd type, long-term climate variation, geographic location (region) and the abattoir*** where animals were processed. Predictions from the model are presented in Fig. 1B.

Conclusions

Liver fluke ***prevalence was high*** at the herd level. However, there was a lower prevalence at the animal level, which may indicate variation in exposure within herds. Within herd prevalence varied significantly in time and space, and by abattoir, herd-type and some climate variables. These data are a useful source of information on a widespread and endemic disease, despite known limitations in terms of performance (low test sensitivity). As well as informing on the distribution and severity of liver fluke infection within herds in Northern Ireland, these analyses will be used to investigate the effect of co-infection with bovine tuberculosis.

Acknowledgements

This study is one component of a larger study investigating concurrent infections (bovine Tuberculosis with liver fluke, BVD and Johne's Disease) in cattle in Northern Ireland funded by the Department of Agriculture and Rural Development (DARD) Project: 15-3-10. www.dardni.gov.uk